SEQUENCE LISTING

<110> Hilton, Douglas J.
      Nicola, Nicos A.
      Farley, Alison
      Wilson, Tracy
      Zhang, Jian-Guo
      Alexander, Warren
      Rakar, Steven
      Fabri, Louis
      Kojima, Tetsuo
      Maeda, Masatsugu
      Kikuchi, Yasufumi
      Nash, Andrew

<120> A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
      ENCODING SAME

<130> DAVIES COLLISON CAVE (CIP)

<140> 09/037,657
<141> 1998-03-10

<150> 08/928,720
<151> 1997-09-11

<160> 54

<170> PatentIn Ver. 2.0

<210> 1
<211> 5
<212> PRT
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<220>
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<400> 1
Trp Ser Xaa Trp Ser
  1   5

<210> 2
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: M116 probe

<400> 2
actcgctcca gattcccgcc tttt   24

<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:M108 probe

<400> 3
tcccgccttt ttcgacccat agat   24

<210> 4
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<212> DNA
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<220>
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<400> 4
ggtacttggc ttggaagagg aaat   24

<210> 5
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<212> DNA
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<400> 5
cggctcacgt gcacgtcggg tggg   24

<210> 6
<211> 22
<212> DNA
<213> Artificial Sequence

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<400> 6
agctgctgtt aaagggcttc tc   22

<210> 7
<211> 15
<212> DNA
<213> Unknown

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<220>
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<222> (1)
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<220>
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<220>
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<400> 7
rctccartcr ctcca                                                    15


<210> 8
<211> 15
<212> DNA
<213> Unknown

<220>
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<222> (1)
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<220>
<221> unsure
<222> (7)
<223> Unsure at position 7

<220>
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<222> (10)
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<400> 8
rctccaytcr ctcca                                                    15


<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:1944 probe
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<400> 9
aagtgtgacc atcatgtgga c   21

<210> 10
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:2106 probe

<400> 10
ggaggtgtta aggaggcg   18

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:2120 probe

<400> 11
atgcccgcgg gtcgcccg   18

<210> 12
<211> 1629
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (124)..(1362)

<220>
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<400> 12
ggcacgagct tcgctgtccg cgcccagtga cgcgcgtgcg gacccgagcc ccaatctgca 60

ccccgcagac tcgcccccgc cccataccgg cgttgcagtc accgcccgtt gcgcgccacc 120

ccc atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg   168
    Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
    1   5   10   15

ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc   216
Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
                20   25   30

ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc   264
Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
                35   40   45

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```
ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc    312
Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
        50              55              60

tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg    360
Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
        65              70              75

acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac    408
Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
 80              85              90              95

acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag    456
Thr Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
                100             105             110

cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg    504
Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
            115             120             125

gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac    552
Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
        130             135             140

atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca    600
Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
        145             150             155

ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag    648
Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
160             165             170             175

tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac    696
Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
            180             185             190

act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc    744
Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
            195             200             205

act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca    792
Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
            210             215             220

aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac    840
Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp
        225             230             235

ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag    888
Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
240             245             250             255

ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc    936
Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
            260             265             270

caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg    984
```

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Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
          275   280   285

aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc   1032
Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
          290   295   300

ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc   1080
Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
          305   310   315

ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac   1128
Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His
320   325   330   335

ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc   1176
Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
                  340   345   350

ggg gtg tgc gag ccg cgg ggc ggc gag ccc agc tcg ggc ccg gtg cgg   1224
Gly Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
              355   360   365

cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc   1272
Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
          370   375   380

tcg aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag   1320
Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
          385   390   395

aag tca cac aag acc cga aac cag gtc ctg ccg gct aaa ctc   1362
Lys Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
400   405   410

taaggatagg ccatcctcct gctgggtcag acctggaggc tcacctgaat tggagcccct 1422

ctgtaccatc tgggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa 1482

ccacagcttt ggtccacatg atggtcacac ttggatatac cccagtgtgg gtaaggttgg 1542

ggtattgcag ggcctcccaa caatctcttt aaataaataa aggagttgtt caggtaaaaa 1602

aaaaaaaaaa aaaaaaaaaa aaaaaaa   1629

<210> 13
<211> 413
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:Murine NR6.1

<400> 13
Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro
 1   5   10   15

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Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
            20   25   30

Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
            35   40   45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
    50   55   60

Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
65   70   75   80

Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
                85   90   95

Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
            100   105   110

Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
            115   120   125

Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
    130   135   140

Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
145   150   155   160

Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
                165   170   175

Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
                180   185   190

Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
            195   200   205

Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
    210   215   220

Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
225   230   235   240

Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
            245   250   255

Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
            260   265   270

Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
    275   280   285

Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
    290   295   300

Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
305   310   315   320

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```
Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
            325               330              335

Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly
            340               345              350

Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
            355               360              365

Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
    370               375              380

Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
385               390              395              400

Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
            405               410
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<210> 14
<211> 1673
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (125)..(1399)

<220>
<223> Description of Unknown Organism:Murine NR6.2

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ggcacgagct tcgctgtccg cgcccagtga cgcgcgtgcg acccgagcc ccaatctgca 60

ccccgcagac tcgcccccgc cccataccgg cgttgcagtc accgcccgtt gcgcgccacc 120

ccca atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg   169
     Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
      1                5                   10                  15

ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc   217
Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
              20               25               30

ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc   265
Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
          35               40                   45

ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc   313
Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
          50               55               60

tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg   361
Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
    65               70                   75

acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac   409
```

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```
Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
 80                     85                  90                      95

acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag    457
Thr Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
                100                 105                 110

cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg    505
Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
                115                 120                 125

gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac    553
Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
                130                 135                 140

atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca    601
Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
                145                 150                 155

ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag    649
Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
160                 165                 170                 175

tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac    697
Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
                180                 185                 190

act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc    745
Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
                195                 200                 205

act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca    793
Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
                210                 215                 220

aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac    841
Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp
    225                 230                 235

ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag    889
Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
240                 245                 250                 255

ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc    937
Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
                260                 265                 270

caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg    985
Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
                275                 280                 285

aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc   1033
Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
                290                 295                 300

ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc   1081
Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
```

```
ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac    1129
Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His
320                 325                 330                 335

ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc    1177
Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
                340                 345                 350

ggg gtg tgc gag ccg cgg ggc ggc gag ccc agc tcg ggc ccg gtg cgg    1225
Gly Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
            355                 360                 365

cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc    1273
Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
            370                 375                 380

tcg aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag    1321
Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
            385                 390                 395

aag tca cac aag acc cga aac cag gac gag ggg atc ctg cct tcg ggc    1369
Lys Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly
400                 405                 410                 415

aga cgg ggt gcg gcg aga ggt cct gcc ggt taaactctaa ggataggcca    1419
Arg Arg Gly Ala Ala Arg Gly Pro Ala Gly
                420                 425

tcctcctgct gggtcagacc tggaggctca cctgaattgg agcccctctg taccatctgg 1479

gcaacaaaga aacctaccag aggctggggc acaatgagct cccacaacca cagctttggt 1539

ccacatgatg gtcacacttg gatatacccc agtgtgggta aggttggggt attgcagggc 1599

ctcccaacaa tctctttaaa taaataaagg agttgttcag gtaaaaaaaa aaaaaaaaaa 1659

aaaaaaaaaa aaaa                                                    1673
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<210> 15
<211> 425
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:Murine NR6.2

<400> 15

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Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro
  1               5                  10                  15

Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
                20                  25                  30

Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
```

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
        50   55   60

Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
65   70   75   80

Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
                85   90   95

Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
            100   105   110

Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
            115   120   125

Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
        130   135   140

Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
145   150   155   160

Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
                165   170   175

Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
            180   185   190

Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
        195   200   205

Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
    210   215   220

Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
225   230   235   240

Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
            245   250   255

Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
            260   265   270

Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
        275   280   285

Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
    290   295   300

Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
305   310   315   320

Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
                325   330   335

Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly

```
                340                      345                          350
Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
        355                     360                 365

Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
    370                 375             380

Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
385                 390                 395                     400

Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg
                405                 410                 415

Arg Gly Ala Ala Arg Gly Pro Ala Gly
            420                 425
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<210> 16
<211> 938
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)..(465)

<220>
<223> Description of Unknown Organism:Murine NR6.3

<400> 16
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ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc ggg atc tat   48
Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
 1               5                   10                  15

ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac ccc acc gct   96
Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
            20                  25                  30

gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc ggg gtg tgc  144
Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly Val Cys
            35                  40                  45

gag ccg cgg ggc ggc gag ccc agc tcg ggc ccg gtg cgg cgc gag ctc  192
Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
    50                  55                  60

aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc tcg aac ctt  240
Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
 65                  70                  75                  80

agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag aag tca cac  288
Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His
                85                  90                  95

aag acc cga aac cag gta gga aag ttg ggg gag gct tgc gtg ggg ggt  336
Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly
```

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```
aaa gga gca gag gaa gag aga gac ccg ggt gag cag cct cca caa cac   384
Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
        115              120                  125

cgc act ctt ctt tcc aag cac agg acg agg gga tcc tgc cct cgg gca   432
Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
    130                  135                  140

gac ggg gtg cgg cga gag gta agg ggg tct ggg tgagtggggc ctacagcagt 485
Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
145                  150                  155

ctagatgagg ccctttcccc tccttcggtg ttgctcaaag ggatctctta gtgctcattt 545

cacccactgc aaagagcccc aggttttact gcatcatcaa gttgctgaag ggtccaggct 605

taatgtggcc tcttttctgc cctcaggtcc tgccggctaa actctaagga taggccatcc 665

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aacaaagaaa cctaccatga ggctggggca caatgagctc ccacaaccac agctttggtc 785

cacatgatgg tcacacttgg atatacccca gtgtgggtaa ggttggggta ttgcagggcc 845

tcccaacaat ctctttaaat aaataaagga gttgttcagg taaaaaaaaa aaaaaaaaaa 905

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa                              938
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<210> 17
<211> 155
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:Murine NR6.3

<400> 17
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Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
 1               5                  10                  15

Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
            20                  25                  30

Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly Val Cys
        35                  40                  45

Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
    50                  55                  60

Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
65                  70                  75                  80

Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His
                85                  90                  95
```

```
Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly
            100                 105             110

Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
        115                 120                 125

Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
    130                 135                 140

Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
145                 150                 155


<210> 18
<211> 834
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(834)

<220>
<223> Description of Artificial Sequence: Nucleotide
      sequence of products generated by 5' RACE of brain
      cDNA using NR6 specific primers

<400> 18
ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc tct ata cat      48
Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
  1               5                  10                  15

gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg acc ctc aat      96
Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
                20                  25                  30

ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac acc tcc acc     144
Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr
            35                  40                  45

ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag cag tca gga     192
Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly
    50                  55                  60

gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg gct ggc tcc     240
Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser
65                  70                  75                  80

tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac atc agc tgc     288
Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys
                85                  90                  95

tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca ccg ggt gca     336
Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala
                100                 105                 110

cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag tac aag ctg     384
```

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```
His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu
        115                 120                 125

agg tgg tac ggt cag gat aac aca tgt gag gag tac cac act gtg ggg      432
Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly
        130                 135                 140

ccc cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc act ccc tat      480
Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr
145                 150                 155                 160

gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca aga tct gat      528
Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp
                165                 170                 175

gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac ccc cca ccc      576
Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro
                180                 185                 190

gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag ctg agt gtg      624
Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
                195                 200                 205

cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc caa gcc aag      672
Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys
        210                 215                 220

tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg aag gtg gtg      720
Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val
225                 230                 235                 240

gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc ctg aag ccc      768
Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro
                245                 250                 255

ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc ggg atc tat      816
Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
                260                 265                 270

ggg tcg aaa aag gcg gga                                              834
Gly Ser Lys Lys Ala Gly
        275


<210> 19
<211> 278
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Haemopoietin receptor

<400> 19
Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
 1                 5                 10                 15

Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
```

```
                    20                      25                      30
Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr
        35                      40                      45

Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly
    50                      55                      60

Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser
 65                      70                      75                  80

Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys
                85                      90                      95

Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala
           100                     105                     110

His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu
        115                     120                     125

Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly
    130                     135                     140

Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr
145                     150                     155                160

Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp
                165                     170                     175

Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro
            180                     185                     190

Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
            195                     200                     205

Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys
    210                     215                     220

Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val
225                     230                     235                240

Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro
            245                     250                     255

Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
            260                     265                     270

Gly Ser Lys Lys Ala Gly
        275


<210> 20
<211> 143
<212> DNA
<213> Artificial Sequence

<220>
```

<221> CDS
<222> (105)..(143)

<220>
<223> Description of Artificial Sequence:Nucleotide
      sequence unique to 5' RACE of brain cDNA

<400> 20
ggcatgaagg cttagggtgg ggatcggtag gacccatgca cccagagaaa gggactggtg 60

gcaactttca aactctctgg ggaaggaaga agggctgaaa gagg atg aac ggg ctc 116
                                                    Met Asn Gly Leu
                                                     1

aga cac agc tgt aat cag ccc cca gga   143
Arg His Ser Cys Asn Gln Pro Pro Gly
  5   10

<210> 21
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino Acid Sequence encoded
by Nucleotide sequence unique to 5' RACE of brain cDNA

<400> 21
Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly
  1   5   10

<210> 22
<211> 1930
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Murine NR6

<400> 22
ggcacgagct tcgctgtccg cgcccagtga cgcgcgtgcg gacccgagcc ccaatctgca 60

ccccgcagac tcgcccccgc cccataccgg cgttgcagtc accgcccgtt gcgcgccacc 120

cccaatgccc gcgggtcgcc cgggccccgt cgcccaatcc gcgcggcggc cgccgcggcc 180

gctgtcctcg ctgtggtcgc ctctgttgct ctgtgtcctc ggggtgcctc ggggcggatc 240

gggagcccac acagctgtaa tcagcccccca ggaccccacc cttctcatcg gctcctccct 300

gcaagctacc tgctctatac atggagacac acctggggcc accgctgagg ggctctactg 360

gaccctcaat ggtcgccgcc tgccctctga gctgtcccgc ctccttaaca cctccaccct 420

ggccctggcc ctggctaacc ttaatgggtc caggcagcag tcaggagaca atctggtgtg 480

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```
tcacgcccga gacggcagca ttctggctgg ctcctgcctc tatgttggct tgcccctga 540

gaagcccttt aacatcagct gctggtcccg gaacatgaag gatctcacgt gccgctggac 600

accgggtgca cacggggaga cattcttaca taccaactac tccctcaagt acaagctgag 660

gtggtacggt caggataaca catgtgagga gtaccacact gtgggccctc actcatgcca 720

tatccccaag gacctggccc tcttcactcc ctatgagatc tgggtggaag ccaccaatcg 780

cctaggctca gcaagatctg atgtcctcac actggatgtc ctggacgtgg tgaccacgga 840

ccccccaccc gacgtgcacg tgagccgcgt tggggggcctg gaggaccagc tgagtgtgcg 900

ctgggtctca ccaccagctc tcaaggattt cctcttccaa gccaagtacc agatccgcta 960

ccgcgtggag gacagcgtgg actggaaggt ggtggatgac gtcagcaacc agacctcctg 1020

ccgtctcgcg ggcctgaagc ccggcaccgt ttacttcgtc caagtgcgtt gtaacccatt 1080

cgggatctat gggtcgaaaa aggcgggaat ctggagcgag tggagccacc ccaccgctgc 1140

ctccacccct cgaagtgagc gcccgggccc gggcggcggg gtgtgcgagc cgcggggcgg 1200

cgagcccagc tcgggcccgg tgcggcgcga gctcaagcag ttcctcggct ggctcaagaa 1260

gcacgcatac tgctcgaacc ttagtttccg cctgtacgac cagtggcgtg cttggatgca 1320

gaagtcacac aagacccgaa accaggtagg aaagttgggg gaggcttgcg tggggggtaa 1380

aggagcagag gaagagagag acccgggtga gcagcctcca caacaccgca ctcttctttc 1440

caagcacagg acgaggggat cctgccctcg ggcagacggg gtgcggcgag aggtaagggg 1500

gtctgggtga gtggggccta cagcagtcta gatgaggccc tttcccctcc ttcggtgttg 1560

ctcaaaggga tctcttagtg ctcatttcac ccactgcaaa gagccccagg ttttactgca 1620

tcatcaagtt gctgaagggt ccaggcttaa tgtggcctct tttctgccct caggtcctgc 1680

cggctaaact ctaaggatag gccatcctcc tgctgggtca gacctggagg ctcacctgaa 1740

ttggagcccc tctgtaccta tctgggcaac aaagaaacct accatgaggc tggggcacaa 1800

tgagctccca caaccacagc tttggtccac atgatggtca cacttggata taccccagtg 1860

tgggtaaggt tggggtattg cagggcctcc caacaatctc tttaaataaa taaaggagtt 1920

gttcaggtaa                                                        1930


<210> 23
<211> 560
<212> DNA
<213> Artificial Sequence

<220>
```

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<400> 23
```
tccaggcagc ggtcggggga caacctcgtg tgccacgccc gtgacggcag catcctggct 60

ggctcctgcc tctatgttgg cctgccccca gagaaacccg tcaacatcag ctgctggtcc 120

aagaacatga aggacttgac ctgccgctgg acgccagggg cccacgggga gaccttcctc 180

cacaccaact actccctcaa gtacaagctt aggtggtatg gccaggacaa cacatgtgag 240

gagtaccaca cagtgggggcc ccactcctgc cacatcccca aggacctggc tctctttacg 300

ccctatgaga tctgggtgga ggccaccaac cgcctgggct ctgcccgctc cgatgtactc 360

acgctggata tcctggatgt ggtgaccacg gacccccccgc ccgacgtgca cgtgagccgc 420

gtcggggggcc tggaggacca gctgagcgtg cgctgggtgt cgccacccgc cctcaaggat 480

ttccttttttc aagccaaata ccagatccgc taccgagtgg aggacagtgt ggaatggaag 540

gtggtggacg atgtgagcaa                                               560
```

<210> 24
<211> 1391
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)..(1050)

<220>

<400> 24
```
acc ctc aac ggg cgc cgc ctg ccc cct gag ctc tcc cgt gta ctc aac    48
Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
 1               5                  10                  15

gcc tcc acc ttg gct ctg gcc ctg gcc aac ctc aat ggg tcc agg cag    96
Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
            20                  25                  30

cgg tcg ggg gac aac ctc gtg tgc cac gcc cgt gac ggc agc atc ctg    144
Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
        35                  40                  45

gct ggc tcc tgc ctc tat gtt ggc ctg ccc cca gag aaa ccc gtc aac    192
Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn
    50                  55                  60

atc agc tgc tgg tcc aag aac atg aag gac ttg acc tgc cgc tgg acg    240
Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
```

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```
cca ggg gcc cac ggg gag acc ttc ctc cac acc aac tac tcc ctc aag   288
Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
                85                  90                  95

tac aag ctt agg tgg tat ggc cag gac aac aca tgt gag gag tac cac   336
Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
            100                 105                 110

aca gtg ggg ccc cac tcc tgc cac atc ccc aag gac ctg gct ctc ttt   384
Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
            115                 120                 125

acg ccc tat gag atc tgg gtg gag gcc acc aac cgc ctg ggc tct gcc   432
Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
    130                 135                 140

cgc tcc gat gta ctc acg ctg gat atc ctg gat gtg gtg acc acg gac   480
Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp
145                 150                 155                 160

ccc ccg ccc gac gtg cac gtg agc cgc gtc ggg ggc ctg gag gac cag   528
Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
                165                 170                 175

ctg agc gtg cgc tgg gtg tcg cca ccc gcc ctc aag gat ttc ctc ttt   576
Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
            180                 185                 190

caa gcc aaa tac cag atc cgc tac cga gtg gag gac agt gtg gac tgg   624
Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
            195                 200                 205

aag gtg gtg gac gat gtg agc aac cag acc tcc tgc cgc ctg gcc ggc   672
Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
            210                 215                 220

ctg aaa ccc ggc acc gtg tac ttc gtg caa gtg cgc tgc aac ccc ttt   720
Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
225                 230                 235                 240

ggc atc tat ggc tcc aag aaa gcc ggg atc tgg agt gag tgg agc cac   768
Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His
                245                 250                 255

ccc aca gcc gcc tcc act ccc cgc agt gag cgc ccg ggc ccg ggc ggc   816
Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
                260                 265                 270

ggg gcg tgc gaa ccg cgg ggc gga gag ccg agc tcg ggg ccg gtg cgg   864
Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
            275                 280                 285

cgc gag ctc aag cag ttc ctg ggc tgg ctc aag aag cac gcg tac tgc   912
Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
    290                 295                 300
```

-20-

```
tcc aac ctc agc ttc cgc ctc tac gac cag tgg cga gcc tgg atg cag    960
Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
305             310             315             320

aag tcg cac aag acc cgc aac cag cac agg acg agg gga tcc tgc cct   1008
Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro
                325             330             335

cgg gca gac ggg gca cgg cga gag gtc ctg cca gat aag ctg          1050
Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu
            340             345             350

taggggctca ggccaccctc cctgccacgt ggagacgcag aggccgaacc caaactgggg 1110

ccacctctgt accctcactt cagggcacct gagcccctca gcaggagctg gggtggcccc 1170

tgagctccaa cggccataac agctctgact cccacgtgag gccacctttg ggtgcacccc 1230

agtgggtgtg tgtgtgtgtg tgagggttgg ttgagttgcc tagaacccct gccagggctg 1290

ggggtgagaa ggggagtcat tactccccat tacctagggc ccctccaaaa gagtcctttt 1350

aaataaatga gctatttagg tgcaaaaaaa aaaaaaaaa a                       1391


<210> 25
<211> 350
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism:    Haemopoietin receptor

<400> 25
Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
 1               5                   10                  15

Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
            20                  25                  30

Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
            35                  40                  45

Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn
     50                  55                  60

Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
 65                  70                  75                  80

Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
                85                  90                  95

Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
            100                 105                 110

Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
            115                 120                 125
```

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```
Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
    130             135             140

Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp
145             150             155             160

Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
            165             170             175

Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
            180             185             190

Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
        195             200             205

Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
    210             215             220

Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
225             230             235             240

Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His
            245             250             255

Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
            260             265             270

Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
        275             280             285

Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
    290             295             300

Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
305             310             315             320

Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro
            325             330             335

Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu
            340             345             350


<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:UP1
      Oligonucleotide

<400> 26
tccaggcagc ggtcggggga caac                                      24


<210> 27
```

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:LP1
     Oligonucleotide

<400> 27
ttgctcacat cgtccaccac cttc   24

<210> 28
<211> 6663
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:Murine NR6 gene

<400> 28
cccagaactc ttggacgctg aggcaggagg attcccaagt ttcaagacag tgtgtttcta 60

ggtaatgaga ccctgtcaag aaaagaaaag aaataaagag acaagaaaat gtttataggc 120

tgtgagacag cttggtgggt aagggcact tgcctccaat caagatgacc tcagccccat 180

ccctaggaat ccatggtaga aggagaaagc aaactcgcag ctgctgacct ccatacatgt 240

gctccaatgt gcacacacac agggagacat aatcaattaa taggatgtat ttgcttagat 300

ttgagtaggc atttatgact gatgttttaa aatttttatt tgattttatg aaaatatacc 360

tgtttgtatt tggtttggtt tggtttgagt tttgtttatt tgagacaggg cttctctgtg 420

tagtcctggc tgtccttgga actcactctg tagaccaggc tggccttgaa ctcagaaatc 480

cgcctgcttg tgcttcccaa gtgcttagat taaaggtgtg cactgccatt cagcaaaatt 540

gcatacttta accccagtat ttgggaggca gaggcagact aatgtgtgaa ttccaggcta 600

gccaaggata cagagtgaga ccctattctt accctcccc cccaaaaccc caaaatgtat 660

tttgtgcttg tgtatgtaca tgtgtgttgc agcacgtaaa tgtccaagga caacttgtag 720

aagttctctc cgttcacagt ctaagtcctg aattcaaact aaggtcctca ggcttagcca 780

cagtcttctt tatgtactga gccatttcac tggccctgga ttgactgatg aattaatttt 840

tgagataagg tctcttgtag ctctagctag gctcaaacta tgaactccca aggtcatctt 900

gagctgctgg tactcttgct tccacccaa gtggtggaat gatactcagg cagcacttct 960

ctggggaagg ggctggcctt ggccttgatt ttgttgcctc agcttcaatg agtgcttggg 1020

tctcgttgtt tcttttcttt atctgtgaaa tgggtgaaca cctgttcaag acttcctgac 1080

-23-

```
tcttgaaaca tccaggcagg gtgagggact tgaagtgggc tcatcccatg cctaacaaag 1140

tgtcgtcttt gaccccagac acagctgtaa tcagcccca ggaccccacc cttctcatcg 1200

gctcctccct gcaagctacc tgctctatac atggagacac acctggggcc accgctgagg 1260

ggctctactg gaccttcaat ggtcgccgcc tgccctctga gctgtcccgc ctccttaaca 1320

cctccaccct ggccctggcc ctggctaacc ttaatgggtc caggcagcag tcaggagaca 1380

atctggtgtg tcacgcccga gacggcagca ttctggctgg ctcctgcctc tatgttggct 1440

gtaagtgggg ccccagacac tcagagatag atgggggttg gcaatgacag atttagagcc 1500

tgggtcttct gtcctggggc agagccatgg gctctcactt gcatgcaggc atggtcatac 1560

ccagcacagg cattgcaact ctagggacag ctgtggctgc actgtcccct gtgtacccca 1620

cagctttaga aaagctgtca tgttttcctt gtagtgcccc ctgagaagcc ctttaacatc 1680

agctgctggt cccggaacat gaaggatctc acgtgccgct ggacaccggg tgcacacggg 1740

gagacattct tacataccaa ctactccctc aagtacaagc tgaggttggt acccagccaa 1800

gccttgctgt gtgacttctg gcaatactta ccttctctga tcaaatatgt tcctgtttat 1860

gaactcaaaa gggactctcg cacctccaca ggtggtacgg tcaggataac acatgtgagg 1920

agtaccacac tgtgggccct cactcatgcc atatccccaa ggacctggcc ctcttcactc 1980

cctatgagat ctgggtggaa gccaccaatc gcctaggctc agcaagatct gatgtcctca 2040

cactggatgt cctggacgtg ggtgagcccc cagtgtccac ctgtgttctg ccctagacct 2100

tatagggcgc ctcccccccca tcccccagaga cttttttggtt cttctagagg tcttagccac 2160

agccacggtg gttgcaggac agtggttgtt cataacttaa tgcaaagact ttcccccaag 2220

acagtcaaga ttttcccct ccccaccccc aacacacaca tacacacaca ctctgcagag 2280

aacacctggc ctgaccaccc tccctctcta cagcccaggt gttcagaagg gagtcctagg 2340

ggactgagag gaggcgccca ggtctgaagg cgccccagga agccgaggcc ttgagctggg 2400

gggggggcg agggttggag gcacgaactg gatgatccct gagcacaact gggcctaatc 2460

taattagggt gttcccagcc caaagcagcc tgggccattt aacccttcaa gtgcctcact 2520

gaagactcag gggagagatc agcttgtact ctctccatgg tcccccagga gggttcctgg 2580

gtgcccctgg ctcattccca catccagagg ttttgtgtct tcctggcatc taaccctcag 2640

ttgtgctctg tggctggcac agctgccccg tggaggctct tggtaatgta caaggcatca 2700

gaggtggaca tgggatgggg atacataggg atggagccaa atagcacctc aaggtggggt 2760

gatatacaat aaagcttgtc accctgacgc tcagaaagcc tactcatgat gatcacaatt 2820
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Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser
        35   40   45

Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser
    50   55   60

Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly

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Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser
                    85   90   95

Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly
            100   105   110

Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys
            115   120   125

Leu Arg Leu Val Arg Ser Glu Xaa His Met Xaa Gly Val Pro His Cys
        130   135   140

Glu Pro Ser Leu Met Pro Tyr Pro Gln Gly Pro Gly Pro Leu His Ser
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Leu Xaa Asp Leu Gly Gly Ser His Gln Ser Pro Arg Leu Ser Lys Ile
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Xaa Cys Pro His Thr Gly Cys Pro Gly Arg
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Oligonucleotide
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ttgagctggg ggggggggcg agggttggag gcacgaactg gatgatccct gagcacaact 7620

gggcctaatc taattagggt gttcccagcc caaagcagcc tgggccattt aacccttcaa 7680

gtgcctcact gaagactcag gggagagatc agcttgtact ctctccatgg tcccccagga 7740

gggttcctgg gtgcccctgg ctcattccca catccagagg ttttgtgtct tcctggcatc 7800
```

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taaccctcag ttgtgctctg tggctggcac agctgccccg tggaggctct tggtaatgta 7860

caaggcatca gaggtggaca tgggatgggg atacataggg atggagccaa atagcacctc 7920

aaggtggggt gatatacaat aaagcttgtc accctgacgc tcagaaagcc tactcatgat 7980

gatcacaatt gttgacatca ctctgggaca tgtagtgaga ccctagctca aaacacagac 8040

agtagcttta agagtcagct tgtgacttaa tactggaact cagggcctaa taggtgctgg 8100

gtgatgctcg cctcactccc tgtttagtga gatctctgcg ctaatctcca ccccagctgg 8160

gtgggctgct ctgtcccctt gagggcagga atgtgtgtct tccatcagag ataggacccg 8220

tggtagcagc aactgctgct ggctgtttct ggaatattaa atgacagtaa tctatcaggc 8280

ctgggtgagt agctaacagg ggtggggggcg tggtctggaa aacgcagata gggtcatagg 8340

agccactgca gcctagatta caccactggg tgttctgtca ctaggccatt ctcaccaagc 8400

agtcctcaga actgggagca ctgttgccag catttaatgc cagcatttaa tgccagcatt 8460

aggggaggca gaggcagaag gatctctctg agttcaaggc catcctgaat ttacataaag 8520

agctccaggc cagccagggt gcgcagtaaa accttgtctc aaaaaacaaa gcatctttag 8580

tgaccaggct tgctccaccc ccagtgacca cggacccccc acccgacgtg cacgtgagcc 8640

gcgttggggg cctggaggac cagctgagtg tgcgctgggt ctcaccacca gctctcaagg 8700

atttcctctt ccaagccaag taccagatcc gctaccgcgt ggaggacagc gtggactgga 8760

aggtgcccgt cccgccccgg acccgcccct gaccccgccc cccgcatctg actcctccct 8820

caccgtgcag gtggtggatg acgtcagcaa ccagacctcc tgccgtctcg cgggcctgaa 8880

gcccggcacc gtttacttcg tccaagtgcg ttgtaaccca ttcgggatct atgggtcgaa 8940

aaaggcggga atctggagcg agtggagcca ccccaccgct gcctccaccc ctcgaagtgg 9000

tgagcacctc tccagggctg gctggcccat ggaatcccca atccatcctg ttccttcccc 9060

cccacccttt ttttgagaca gcgtcttcag gtagcgcatg ctggccttaa attcagtatg 9120

tagtcaagga tgacctcgag ctcctggtct ttttgtctcc acttagagac aatggccagt 9180

ggccatcacc acctttggga gactagccat ggagtctatt tagcctgtca tttggtgaca 9240

gatggagtac aacagtgtga cctcttgtaa gagaactgaa gacaggctgt ttttaacccc 9300

aatatcctag ctctctaga ggttaacttt atataaaata gagactatta cagccagtta 9360

tcacatggtc ccacagaacc ttttgtcaca caacctatag accacagtgc ctgtgcctac 9420

cacataaggg tctctactgc tggcccaccc ctccaaccct taaaaggtaa cctaggcagc 9480

cttaatattt gcaatcctcc tacctcagcc tcttgaatgc tcagaaacca ggcattaacc 9540
```

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```
caagtttctc ttctctgggt ccctttctta aggtgggagg gcctaaagat gacttccttt 9600

gtcctgaaga ctctccgagc ccatggatct gcactctcta atatgaaata tattgcataa 9660

aatgtctggc ctcagtttcc ccacctgtca ggtttaggca gcacagtcgg tccaagacac 9720

ttcattattt gcaggcagta taagaagaag ctcccatccc ccacccgctt cctccggtcc 9780

ctaagacaga atacttctac actgaaactg aactctcgca gacgcatatg ctcactttaa 9840

tgatgatgaa ataatgggga aactgaggct ccgagagatt cctggaggaa gagggtcaaa 9900

accagctcca ggaagctctc cagcccccat ccgggcctct ccaggttctg ggcttggcgg 9960

gagtgaacac agctgggagg ggctggagcc tgggagcttt ggcccttgct cgtgcccagc 10020

acctgcgatt cttgcacggg agccagcagg cggctgcgtc cgcccgagag actgaagaag 10080

ccggggggtag ggttggaggg aggtaagcag gggctgtggg ggccgaagct tgtgccaggg 10140

cctgtcagcg agtccccagt tttatttatg gcgtgaggcc gatgtcctta tccgctggcc 10200

tgctggggga tggctgcggc tggggattgg acccaagggc tggcttccca ctcagtcctc 10260

cagcccactc catgtcacac ccgtgcattc tctgaggctt atcttgggaa cccgcccttg 10320

ttctgtgctg tctgtctcta tttctgtcat tcactttccc agagcctttt ttttatgctt 10380

ttaatataac tacgttttaa aaattgcttt tgtataatgt gtgtgccttc gtgagcgtgc 10440

gtgccacaac acacacgtga aggttagaga actttgttga gtaggctcct tccaccatgt 10500

gggactaggg ctggcgacaa gagcaattac tgagtcatct cgccagcccc tcacccctca 10560

cttcccatcc tgtttggata gtcataggta atcgaaggta aatcgctggc tttaatttcg 10620

tagctatcct gcctcagcct accaagtgct gtgctaccac gtttgtggga ggggctctcc 10680

tcccagtgtc tgggggtaca cagtcccaag atctctgctt tctaggtctt tgtcttagtt 10740

tgccccttgc tttgtccgtg tccctagagt ctccggcccc acttagtctc cattgatttc 10800

ctttctgacc gaatactcgg ttttacctcc cactgatttg actccctcct ttgcttgtct 10860

ccatcgccgt ggcattgcca ttcctctggg tgactctggg tccacacctg acacctttcc 10920

caactttccc cagccgaagc tggtctggta tgggaggccg ccgtcccgcg cgcgcctcct 10980

gctggccgcg ccccaacact gccgctccat tctctttaga gcgcccgggc ccgggcggcg 11040

gggtgtgcca gccgcggggc ggcgagccca gctcgggccc ggtgcggcgc gagctcaagc 11100

agttcctcgg ctggctcaag aagcacgcat actgctcgaa ccttagtttc cgcctgtacg 11160

accagtggcg tgcttggatg cagaagtcac acaagacccg aaaccaggta ggaaagttgg 11220

gggaggcttg cgtggggggt aaaggagcag aggaagagag agacccgggt gagcagcctc 11280
```

```
cacaacaccg cactcttctt tccaagcaca ggacgagggg atcctgccct cgggcagacg 11340

gggtgcggcg agaggtaagg gggtctgggt gagtggggcc tacagcagtc tagatgaggc 11400

cctttcccct ccttcggtgt tgctcaaagg gatctcttag tgctcatttc acccactgca 11460

aagagcccca ggttttactg catcatcaag ttgctgaagg gtccaggctt aatgtggcct 11520

cttttctgcc ctcaggtcct gccggctaaa ctctaaggat aggccatcct cctgctgggt 11580

cagacctgga ggctcacctg aattggagcc cctctgtacc atctgggcaa caaagaaacc 11640

taccagaggc tgggcacaat gagctcccac aaccacagct ttggtccaca tgatggtcac 11700

acttggatat accccagtgt gggtagggtt ggggtattgc agggcctccc aagagtctct 11760

ttaaataaat aaaggagttg ttcaggtccc gatggccagt gtgtttgggg cctatgtgct 11820

ggggtggggg ga                                                    11832
```

<210> 39
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Murine peptide

<400> 39

```
Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln
 1               5                  10                  15

Ala Thr Cys Ser Ile His Gly Asp Thr Pro
            20                  25
```

<210> 40
<211> 21
<212> DNA
<213> Oligonucleotide Sequence

<400> 40

```
gtccaagtgc gttgtaaccc a                                            21
```

<210> 41
<211> 24
<212> DNA
<213> Oligonucleotide Sequence

<400> 41

```
gctgagtgtg cgctgggtct cacc                                        24
```

<210> 42

<211> 18
<212> DNA
<213> Oligonucleotide Sequence

<400> 42
ggctccactc gctccaga   18

<210> 43
<211> 2079
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (513)..(1775)

<220>
<223> Description of Unknown Organism: Nucleotide Sequence of NR6

<400> 43
gcggtatttg tgtttcaaat ctatctacag aaaagattga gaaccagaag ccctttтcgt 60

tttttgaaag ctagctgact cactgttcaa gaaaggagaa cactttcaat tatgctgttt 120

gactgcagtg tcagggatcc aaaggaaatg actccatccc ttcccttтca tcccaacctc 180

agtgacagca aattctgatg tgactgaggg ttggcttgtg aaggagtcat taggaaattc 240

tgcctaagcc atagcgcgat gagaaggatg tatcctatgg tggtgatttt cctgtgcccc 300

ctcagaggaa agttgtcaga tgagcaggtg gagtattcta tagcaaacag caagctaata 360

ggttacacag ataactctct gactttgcct tacagaacct gtgctattga ccttagggca 420

aggttcatgc tcaggggggcc aactctgtgg gttaggattt gagtttaagc agcttctgct 480

catatttcag cgcccccggc agcgccggcc cc atg ccc gcc ggc cgc cgg ggc   533
                                     Met Pro Ala Gly Arg Arg Gly
                                      1   5

ccc gcc gcc caa tcc gcg cgg cgg ccg ccg ccg ttg ctg ccc ctg ctg   581
Pro Ala Ala Gln Ser Ala Arg Arg Pro Pro Pro Leu Leu Pro Leu Leu
         10   15   20

ctg ctc tgc gtc ctc ggg gcg ccg cga gcc gga tca gga gcc cac aca   629

```
Leu Leu Cys Val Leu Gly Ala Pro Arg Ala Gly Ser Gly Ala His Thr
    25                  30                  35

gct gtg atc agt ccc cag gat ccc acg ctt ctc atc ggc tcc tcc ctg      677

Ala Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu
 40                  45                  50                  55

ctg gcc acc tgc tca gtg cac gga gac cca cca gga gcc acc gcc gag      725

Leu Ala Thr Cys Ser Val His Gly Asp Pro Pro Gly Ala Thr Ala Glu
             60                  65                  70

ggc ctc tac tgg acc ctc aat ggg cgc cgc ctg ccc cct gag ctc tcc      773

Gly Leu Tyr Trp Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser
             75                  80                  85

cgt gta ctc aac gcc tcc acc ttg gct ctg gcc ctg gcc aac ctc aat      821

Arg Val Leu Asn Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn
             90                  95                  100

ggg tcc agg cag cgg tcg ggg gac aac ctc gtg tgc cac gcc cgt gac      869

Gly Ser Arg Gln Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp
    105                 110                 115

ggc agc atc ctg gct ggc tcc tgc ctc tat gtt ggc ctg ccc cca gag      917

Gly Ser Ile Leu Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu
120                 125                 130                 135

aaa ccc gtc aac atc agc tgc tgg tcc aag aac atg aag gac ttg acc      965

Lys Pro Val Asn Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr
                140                 145                 150

tgc cgc tgg acg cca ggg gcc cac ggg gag acc ttc ctc cac acc aac     1013

Cys Arg Trp Thr Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn
             155                 160                 165

tac tcc ctc aag tac aag ctt agg tgg tat ggc cag gac aac aca tgt     1061

Tyr Ser Leu Lys Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys
     170                 175                 180

gag gag tac cac aca gtg ggg ccc cac tcc tgc cac atc ccc aag gac     1109

Glu Glu Tyr His Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp
    185                 190                 195

ctg gct ctc ttt acg ccc tat gag atc tgg gtg gag gcc acc aac cgc     1157

Leu Ala Leu Phe Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg
200                 205                 210                 215
```

```
ctg ggc tct gcc cgc tcc gat gta ctc acg ctg gat atc ctg gat gtg    1205

Leu Gly Ser Ala Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val
                220             225             230

gtg acc acg gac ccc ccg ccc gac gtg cac gtg agc cgc gtc ggg ggc    1253

Val Thr Thr Asp Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly
                235             240             245

ctg gag gac cag ctg agc gtg cgc tgg gtg tcg cca ccc gcc ctc aag    1301

Leu Glu Asp Gln Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys
            250             255             260

gat ttc ctc ttt caa gcc aaa tac cag atc cgc tac cga gtg gag gac    1349

Asp Phe Leu Phe Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp
        265             270             275
agt gtg gac tgg aag gtg gtg gac gat gtg agc aac cag acc tcc tgc    1397

Ser Val Asp Trp Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys
280                 285             290             295

cgc ctg gcc ggc ctg aaa ccc ggc acc gtg tac ttc gtg caa gtg cgc    1445

Arg Leu Ala Gly Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg
                300             305             310

tgc aac ccc ttt ggc atc tat ggc tcc aag aaa gcc ggg atc tgg agt    1493

Cys Asn Pro Phe Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser
                315             320             325

gag tgg agc cac ccc aca gcc gcc tcc act ccc cgc agt gag cgc ccg    1541

Glu Trp Ser His Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro
            330             335             340

ggc ccg ggc ggc ggg gcg tgc gaa ccg cgg ggc gga gag ccg agc tcg    1589

Gly Pro Gly Gly Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser
    345             350             355

ggg ccg gtg cgg cgc gag ctc aag cag ttc ctg ggc tgg ctc aag aag    1637

Gly Pro Val Arg Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys
360             365             370             375

cac gcg tac tgc tcc aac ctc agc ttc cgc ctc tac gac cag tgg cga    1685

His Ala Tyr Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg
            380             385             390

gcc tgg atg cag aag tcg cac aag acc cgc aac cag gac gag ggg atc    1733

Ala Trp Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile
```

ctg ccc tcg ggc aga cgg ggc acg gcg aga ggt cct gcc aga   1775

Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro Ala Arg
        410   415   420

taagctgtag gggctcaggc caccctccct gccacgtgga gacgcagagg ccgaacccaa 1835

actggggcca cctctgtacc ctcacttcag ggcacctgag ccaccctcag caggagctgg 1895

ggtggcccct gagctccaac ggccataaca gctctgactc ccacgtgagg ccacctttgg 1955

gtgcacccca gtgggtgtgt gtgtgtgtgt gagggttggt tgagttgcct agaacccctg 2015

ccagggctgg gggtgagaag gggagtcatt actccccatt acctagggcc cctccaaaag 2075

atcc   2079

<210> 44
<211> 421
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Amino Acid Sequence of NR6

<400> 44
Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg Pro
 1   5   10   15

Pro Pro Leu Leu Pro Leu Leu Leu Leu Cys Val Leu Gly Ala Pro Arg
            20   25   30

Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro Gln Asp Pro Thr
        35   40   45

Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys Ser Val His Gly Asp
    50   55   60

Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn Gly Arg
65   70   75   80

Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn Ala Ser Thr Leu Ala
                85   90   95

Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Arg Ser Gly Asp Asn
            100   105   110

Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser Cys Leu
        115   120   125

```
Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn Ile Ser Cys Trp Ser
    130             .       135         140

Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala His Gly
145             150             155                 160

Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu Arg Trp
                165             170  .              175

Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly Pro His
            180             185             190

Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr Glu Ile
        195         .       200             205

Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp Val Leu
    210             215             220

Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp Pro Pro Pro Asp Val
225             230             235             240

His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val Arg Trp
            245             250             255

Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys Tyr Gln
        260             265             270

Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val Asp Asp
        275             280             285

Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro Gly Thr
    290             295             300

Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr Gly Ser
305             310             315             320

Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala Ala Ser
            325             330             335

Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly Ala Cys Glu Pro
        340             345             350

Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu Lys Gln
        355             360             365

Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu Ser Phe
    370             375             380

Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His Lys Thr
385             390             395             400

Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg Arg Gly Thr Ala
            405             410             415

Arg Gly Pro Ala Arg
        420
```

<210> 45
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Fwd Primer

<400> 45
tgcccccaga gaaacccgtc aac   23

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Rev Primer

<400> 46
cgtgagtaca tcggagcggg cagag   25

<210> 47
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 47
tcaggcgcgc cttgcccaca cagctgtgat c   31

<210> 48
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 48
tcagggcgcg ccttatctgg caggacctct   30

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 49
tcaggcgcgc ctgcccgccg gccgc   25

<210> 50
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 50
ataaggcgcg ccctggcagg acctctcg   28

<210> 51
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 51
tcaggcgcgc cttgcccaca cagctgtgat c   31

<210> 52
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 52
tcagggcgcg ccttatctgg caggacctct   30

<210> 53
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 53

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tcaggcgcgc ctgcccgccg gccgc   25

<210> 54
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 54
ataaggcgcg ccctggcagg acctctcg   28